

## GaMYB1\_alignment\_and\_sequence.txt

## Exhibit 2

gi|7438345|pir||T09879 myb-related protein A - upland cotton  
gi|437327|gb|AAA33067.1| MYB1 [Gossypium hirsutum]  
gi|23476277|gb|AAN28269.1| myb-like transcription factor 1 [Gossypium hirsutum]

Length = 294  
Score = 602 bits (1553), Expect = e-171  
Identities = 288/294 (97%), Positives = 291/294 (98%)  
Frame = +3

Query: 144	MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY	323
Sbjct: 1	MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY	60
Query: 324	LRPDLKRGNFTEEEDELIICKHSSLGNKWSIAGRLPGRTDNEIKNYWNTHIKRKLISRG	503
Sbjct: 61	LRPDLKRGNFTEEEDELIICKHSSLGNKWSIAGRLPGRTDNEIKNYWNTHIKRKLISRG	120
Query: 504	IDPQTHRPLNQTAITNTVTGPTELDFRNSPTSVSKSSIKNPSLDFNYNEFHKSHDSL	683
Sbjct: 121	IDPQTHRPLNQTA TNTVT PTTELDFRNSPTSVSKSSIKNPSLDFNYNEF FKS+TDSL	180
Query: 684	EENCTASTGTTDEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK	863
Sbjct: 181	EENCTAS+GTTDEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVS+ANSAESK	240
Query: 864	PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS	1025
Sbjct: 241	PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS	294

>Contig20 GaMYB1  
GGCACGAGACAGTTCTTTTGTCTCATCCATCATCCCCATGTCCC  
CTCTCCATGTTTCTAAATCTCTCCATATAACCTATAACACCGTTATTCT  
TTCTCTATTCTACCTGATTGATTGATTGTAACTGATGGGAC  
GATCACCTTGTGAAAAGGCTCATACCAACAAAGGTGCCTGGACAAA  
GAGGAAGATCAACGCCATCAACTACATCCGTGTCATGGTGAAGGCTG  
CTGGCGTCCCTCCCCAAAGCTGCTGGCTGCTTAGATGTGGTAAGAGTT  
GCAGATTAAGATGGATAAAACTACTTGAGGCCATCTTAAGAGAGGAAAT  
TTCACTGAAGAAGAAGATGAGCTTATCATCAAGCTTACAGTTACTTGG  
AAACAAATGGTATTGATTGCTGGAAAGATTACAGGAAGGACAGATAATG  
AGATAAAGAAACTACTGGAACACACACATCAAAGAAAGCTTATAAGCAGA  
GGAATTGATCCACAAACTCATCGTCCTCTCAATCAAACGGCCATTACCAA  
CACAGTCACAGGCCACCGAATTGGATTCAAGAAACTCGCCACATCCG  
TTTCCAAATCCAGTTCCATCAAAACCCGTCTGGATTCAATTACAAT  
GAATTTCATTCAGTCCCACACAGATTCCCTTGAAAGAACCAACTGTAC  
AGCCAGCACTGGCATGACTACAGATGAAAGAACACAAGAACAGTCGACA  
AGAAGCAGCAATACGGTCCGAGCAATTGGCAAGACATAAATTGGAGCTG  
TCGATTGGATTGTTAGCTGACTCATCTCGGGTATCAAGTGCCAACCTC  
GGCGAGTCGAAACCAAGGTAGATAACAAACATTCCAGTTCTGAAC  
AAGCTATGGTGGCTAAGGCGGTATGTTGTGGCAATTAGGTTTGGAA  
ACAAGTGAATTGGTAGGAACTGTCAAATTCAAATGGCTTCTA  
TAGTTATTGTAGACCCCTGGATTCATAGGGTCATCTTTCTCTTCTT  
TCTGTTTTAGGAGATAAAATTAAATTCTTAATTATTATCTTTTGCCTGCC  
CACTGTAATCAAAGAAAATTATAAAACAAAGACTCTTTTGTATTGTT  
AAATTATAGGTTAAAAAAAAAAAAAAAAAAAAAA

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>Contig20\_Frame+3 GaMYB1

HETVSLFCFPSSPCPLSMFF\*ISPYTYNTVILSLFYLI\*FDLIL\*LMGRSPCCEKAHTN  
KGAWTKEEDQRLINYIRVHGEGLPGRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE  
EDELIKLHSLGNKWSLIAGRPLGRTDNEIKNYWNTHIKRKLISRGIDPQTHRPLNQTA  
ITNTVTGPTELDFRNSPTSVKSSSIKNPSLDFNYNEFKSHTDSLEEPNCTASTGMTT  
DEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESPKVVDNNNFQFLEQ  
AMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS\*GHLFLLSFCF\*EIN\*FLI  
IIFLPAHCNQSKIKQRLFLICSIYRFKKKKK

>GaMYB1 - putative from GhMYB1 alignment

MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEGLPGRSLPKAAGLLRCGKSCRLRWINY  
LRPDLKRGNFTEEEDELIKLHSLGNKWSLIAGRPLGRTDNEIKNYWNTHIKRKLISRG  
IDPQTHRPLNQTAITNTVTGPTELDFRNSPTSVKSSSIKNPSLDFNYNEFKSHTDSL  
EEPNCTASTGMTTDEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK  
PKVVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS